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TECH CENTER 1600/2900



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/517,491

DATE: 02/28/2002

TIME: 14:57:34

Input Set : N:\Crf3\RULE60\09517491.raw

Output Set: N:\CRF3\02282002\I517491.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Berlin, Vivian
6 Chiu, Maria Isabel
7 Cottarel, Guillaume
8 Damagnez, Veronique
10 (ii) TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
12 (iii) NUMBER OF SEQUENCES: 35
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
16 (B) STREET: One Post Office Square
17 (C) CITY: Boston
18 (D) STATE: MA
19 (E) COUNTRY: USA
20 (F) ZIP: 02109-2170
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/517,491
C--> 30 (B) FILING DATE: 02-Mar-2000
31 (C) CLASSIFICATION:
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/360,144
35 (B) FILING DATE: 20-DEC-1994
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Vincent, Matthew P.
41 (B) REGISTRATION NUMBER: 36,709
42 (C) REFERENCE/DOCKET NUMBER: APV-036.02
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 617-832-1000
46 (B) TELEFAX: 617-832-7000
49 (2) INFORMATION FOR SEQ ID NO: 1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 486 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: both
55 (D) TOPOLOGY: linear
57 (ii) MOLECULE TYPE: cDNA
60 (ix) FEATURE:
61 (A) NAME/KEY: CDS

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```

62          (B) LOCATION: 1..486
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 CTC ACC CGT CAC AAT GCA GCC AAC AAG ATC TTG AAG AAC ATG TGT GAA      48
68 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
69   1          5          10          15
71 CAC AGC AAC ACG CTG GTC CAG CAG GCC ATG ATG GTG AGT GAA GAG CTG      96
72 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
73          20          25          30
75 ATT CGG GTA GCC ATC CTC TGG CAT GAG ATG TGG CAT GAA GGC CTG GAA      144
76 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
77          35          40          45
79 GAG GCA TCT CGC TTG TAC TTT GGG GAG AGG AAC GTG AAA GGC ATG TTT      192
80 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
81          50          55          60
83 GAG GTG CTG GAG CCC CTG CAT GCT ATG ATG GAA CGG GGT CCC CGG ACT      240
84 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
85 65          70          75          80
87 CTG AAG GAA ACA TCC TTT AAT CAG GCA TAT GGC CGA GAT TTA ATG GAG      288
88 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
89          85          90          95
91 GCA CAA GAA TGG TGT CGA AAG TAC ATG AAG TCG GGG AAC GTC AAG GAC      336
92 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
93          100          105          110
95 CTC ACG CAA GCC TGG GAC CTC TAC TAT CAC GTG TTC AGA CGG ATC TCA      384
96 Leu Thr Gln Ala Trp Asp Leu Tyr His Val Phe Arg Arg Ile Ser
97          115          120          125
99 AAG CAG CTA CCC CAG CTC ACA TCC CTG GAG CTG CAG TAT GTG TCC CCC      432
100 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
101          130          135          140
103 AAA CTT CTG ATG TGC CGA GAC CTT GAG TTG GCT GTG CCA GGA ACA TAC      480
104 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
105 145          150          155          160
107 GAC CCC      486
108 Asp Pro
112 (2) INFORMATION FOR SEQ ID NO: 2:
114      (i) SEQUENCE CHARACTERISTICS:
115          (A) LENGTH: 162 amino acids
116          (B) TYPE: amino acid
117          (D) TOPOLOGY: linear
119      (ii) MOLECULE TYPE: protein
121      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
123 Leu Thr Arg His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu
124   1          5          10          15
126 His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu
127          20          25          30
129 Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu
130          35          40          45
132 Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe
133          50          55          60

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```

135 Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Arg Thr
136 65 70 75 80
138 Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu
139 85 90 95
141 Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp
142 100 105 110
144 Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser
145 115 120 125
147 Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro
148 130 135 140
150 Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr
151 145 150 155 160

```

153 Asp Pro

156 (2) INFORMATION FOR SEQ ID NO: 3:

158 (i) SEQUENCE CHARACTERISTICS:

159 (A) LENGTH: 40 base pairs

160 (B) TYPE: nucleic acid

161 (C) STRANDEDNESS: single

162 (D) TOPOLOGY: linear

W--> 164 (ii) MOLECULE TYPE: DNA

168 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

170 GGGTTTGGAA TTCCTAATAA TGTCTGTACA AGTAGAAACC 40

172 (2) INFORMATION FOR SEQ ID NO: 4:

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 34 base pairs

176 (B) TYPE: nucleic acid

177 (C) STRANDEDNESS: single

178 (D) TOPOLOGY: linear

W--> 180 (ii) MOLECULE TYPE: DNA

184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

186 GGGTTTCGGG ATCCCGTCAT TCCAGTTTGA GAAC 34

188 (2) INFORMATION FOR SEQ ID NO: 5:

190 (i) SEQUENCE CHARACTERISTICS:

191 (A) LENGTH: 348 base pairs

192 (B) TYPE: nucleic acid

193 (C) STRANDEDNESS: single

194 (D) TOPOLOGY: linear

196 (ii) MOLECULE TYPE: cDNA

199 (ix) FEATURE:

200 (A) NAME/KEY: CDS

201 (B) LOCATION: 14..325

204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

206 GGAATTCCTA ATA ATG TCC GTA CAA GTA GAA ACC ATC TCC CCA GGA GAC 49

207 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp

208 1 5 10

210 GGG CGC ACC TTC CCC AAG CGC GGC CAG ACC TGC GTG GTG CAC TAC ACC 97

211 Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr

212 15 20 25

214 GGG ATG CTT GAA GAT GGA AAG AAA TTT GAT TCC TCC CGT GAC CGT AAC 145

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215 Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn
216      30                      35                      40
218 AAG CCC TTT AAG TTT ATG CTA GGC AAG CAG GAG GTG ATC CGA GGC TGG      193
219 Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp
220  45                      50                      55                      60
222 GAA GAA GGG GTT GCC CAG ATG AGT GTG GGT CAG CGT GCC AAA CTG ACT      241
223 Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr
224      65                      70                      75
226 ATA TCT CCA GAT TAT GCC TAT GGT GCC ACT GGG CAC CCA GGC ATC ATC      289
227 Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile
228      80                      85                      90
230 CCA CCA CAT GCC ACT CTC GTC TTC GAT GTG GAG CTT CTAAACTGG      335
231 Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
232      95                      100
234 AATGACGGGA TCC      348
237 (2) INFORMATION FOR SEQ ID NO: 6:
239   (i) SEQUENCE CHARACTERISTICS:
240       (A) LENGTH: 104 amino acids
241       (B) TYPE: amino acid
242       (D) TOPOLOGY: linear
244   (ii) MOLECULE TYPE: protein
246   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
248 Met Ser Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
249  1      5      10      15
251 Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
252      20      25      30
254 Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
255      35      40      45
257 Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
258      50      55      60
260 Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
261  65      70      75      80
263 Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
264      85      90      95
266 Thr Leu Val Phe Asp Val Glu Leu
267      100
270 (2) INFORMATION FOR SEQ ID NO: 7:
272   (i) SEQUENCE CHARACTERISTICS:
273       (A) LENGTH: 48 base pairs
274       (B) TYPE: nucleic acid
275       (C) STRANDEDNESS: single
276       (D) TOPOLOGY: linear
W--> 278   (ii) MOLECULE TYPE: DNA
282   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
284 TCGCCGGAAT TCGGGGCGG AGGTGAGGA GTACAAGTAG AAACCATC      48
286 (2) INFORMATION FOR SEQ ID NO: 8:
288   (i) SEQUENCE CHARACTERISTICS:
289       (A) LENGTH: 34 base pairs
290       (B) TYPE: nucleic acid

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291          (C) STRANDEDNESS: single
292          (D) TOPOLOGY: linear
W--> 294      (ii) MOLECULE TYPE: DNA
298          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
300 GGGTTTCGGG ATCCCGTCAT TCCAGTTTGA GAAG          34
302 (2) INFORMATION FOR SEQ ID NO: 9:
304      (i) SEQUENCE CHARACTERISTICS:
305          (A) LENGTH: 41 base pairs
306          (B) TYPE: nucleic acid
307          (C) STRANDEDNESS: single
308          (D) TOPOLOGY: linear
W--> 310      (ii) MOLECULE TYPE: DNA
314          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
316 CGCGGATCCG CGCATTATTA CTTGTTTGA TTGATTTT G          41
318 (2) INFORMATION FOR SEQ ID NO: 10:
320      (i) SEQUENCE CHARACTERISTICS:
321          (A) LENGTH: 40 base pairs
322          (B) TYPE: nucleic acid
323          (C) STRANDEDNESS: single
324          (D) TOPOLOGY: linear
W--> 326      (ii) MOLECULE TYPE: DNA
330          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
332 CGCGGATCCG CGTAAAAGCA AAGTACTATC AATTGAGCCG          40
335 (2) INFORMATION FOR SEQ ID NO: 11:
337      (i) SEQUENCE CHARACTERISTICS:
338          (A) LENGTH: 5430 base pairs
339          (B) TYPE: nucleic acid
340          (C) STRANDEDNESS: both
341          (D) TOPOLOGY: linear
343      (ii) MOLECULE TYPE: cDNA
346      (ix) FEATURE:
347          (A) NAME/KEY: CDS
348          (B) LOCATION: 1..5427
351          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
353 TTG GAG CAC AGT GGG ATT GGA AGA ATC AAA GAG CAG AGT GCC CGC ATG          48
354 Leu Glu His Ser Gly Ile Gly Arg Ile Lys Glu Gln Ser Ala Arg Met
355 1      5      10      15
357 CTG GGG CAC CTG GTC TCC AAT GCC CCC CGA CTC ATC CGC CCC TAC ATG          96
358 Leu Gly His Leu Val Ser Asn Ala Pro Arg Leu Ile Arg Pro Tyr Met
359      20      25      30
361 GAG CCT ATT CTG AAG GCA TTA ATT TTG AAA CTG AAA GAT CCA GAC CCT          144
362 Glu Pro Ile Leu Lys Ala Leu Ile Leu Lys Leu Lys Asp Pro Asp Pro
363      35      40      45
365 GAT CCA AAC CCA GGT GTG ATC AAT AAT GTC CTG GCA ACA ATA GGA GAA          192
366 Asp Pro Asn Pro Gly Val Ile Asn Asn Val Leu Ala Thr Ile Gly Glu
367      50      55      60
369 TTG GCA CAG GTT AGT GGC CTG GAA ATG AGG AAA TGG GTT GAT GAA CTT          240
370 Leu Ala Gln Val Ser Gly Leu Glu Met Arg Lys Trp Val Asp Glu Leu
371 65      70      75      80

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/517,491

DATE: 02/28/2002

TIME: 14:57:36

Input Set : N:\Crf3\RULE60\09517491.raw

Output Set: N:\CRF3\02282002\I517491.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:164 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:180 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
L:278 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:294 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:310 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:326 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:1705 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21
L:1721 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22
L:1775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1835 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:1858 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:1875 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:1892 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:1909 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:1926 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:1943 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:1960 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:1977 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33
L:1994 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:2021 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35